



#9

SUBSTITUTE SEQUENCE LISTING

<110> Xia, Yu-Ping et al.

<120> METHODS FOR TREATING INFLAMMATORY SKIN DISEASES

<130> REG 710b

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<160> 27

<170> PatentIn version 3.0

<210> 1

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 1

gactagcagt ccggaggttag accttttcgta gagatg

36

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<211> 33

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<213> Artificial Sequence

<220>

<223> Primer

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cggactcaga accacatcta tgattgtatt ggt

33

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<211> 35

<212> DNA

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<220>

<223> Primer

<400> 3

acaatcatag atgtggttct gagtccgtct catgg

35

<210> 4

<211> 38

<212> DNA

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<223> Primer

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gataatgccc gggccctttt catggaccct gacaaatg

38

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<220>
<223> Primer

<400> 5
gactagcagt ccggaggtag acctttcgta gagatg

36

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<400> 6
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38

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<220>
<223> Primer

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atccagctgt tgcccaggaa gtcgctggag ctgctggta

39

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<211> 39
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<220>
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<400> 8
attttcatgc acaatgacct cggtgctctc ccgaaatcg

39

<210> 9
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
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<400> 9
tcatagatat ccagctgttg cccaggaagt cgctggag

38

<210> 10
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<220>
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<400> 10
 gataatgccccc gggccatttt catgcacaat gacctcggt

39

<210> 11
 <211> 1704
 <212> DNA
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<220>
 <223> Flt1(1-3)-Fc

<220>
 <221> CDS
 <222> (1)..(1704)

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 Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
 1 5 10 15

48

tgt ctg ctt ctc aca gga tct agt tca ggt tca aaa tta aaa gat cct
 Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro
 20 25 30

96

gaa ctg agt tta aaa ggc acc cag cac atc atg caa gca ggc cag aca
 Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr
 35 40 45

144

ctg cat ctc caa tgc agg ggg gaa gca gcc cat aaa tgg tct ttg cct
 Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro
 50 55 60

192

gaa atg gtg agt aag gaa agc gaa agg ctg agc ata act aaa tct gcc
 Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala
 65 70 75 80

240

tgt gga aga aat ggc aaa caa ttc tgc agt act tta acc ttg aac aca
 Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr
 85 90 95

288

gct caa gca aac cac act ggc ttc tac agc tgc aaa tat cta gct gta
 Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val
 100 105 110

336

cct act tca aag aag aag gaa aca gaa tct gca atc tat ata ttt att
 Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile
 115 120 125

384

agt gat aca ggt aga cct ttc gta gag atg tac agt gaa atc ccc gaa
 Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu
 130 135 140

432

att	ata	cac	atg	act	gaa	gga	agg	gag	ctc	gtc	att	ccc	tgc	cgg	gtt	480
Ile	Ile	His	Met	Thr	Glu	Gly	Arg	Glu	Leu	Val	Ile	Pro	Cys	Arg	Val	
145					150				155						160	
acg	tca	cct	aac	atc	act	gtt	act	tta	aaa	aag	ttt	cca	ctt	gac	act	528
Thr	Ser	Pro	Asn	Ile	Thr	Val	Thr	Leu	Lys	Lys	Phe	Pro	Leu	Asp	Thr	
				165					170					175		
ttg	atc	cct	gat	gga	aaa	cgc	ata	atc	tgg	gac	agt	aga	aag	ggc	ttc	576
Leu	Ile	Pro	Asp	Gly	Lys	Arg	Ile	Ile	Trp	Asp	Ser	Arg	Lys	Gly	Phe	
			180					185						190		
atc	ata	tca	aat	gca	acg	tac	aaa	gaa	ata	ggg	ctt	ctg	acc	tgt	gaa	624
Ile	Ile	Ser	Asn	Ala	Thr	Tyr	Lys	Glu	Ile	Gly	Leu	Leu	Thr	Cys	Glu	
		195					200					205				
gca	aca	gtc	aat	ggg	cat	ttg	tat	aag	aca	aac	tat	ctc	aca	cat	cga	672
Ala	Thr	Val	Asn	Gly	His	Leu	Tyr	Lys	Thr	Asn	Tyr	Leu	Thr	His	Arg	
	210					215					220					
caa	acc	aat	aca	atc	ata	gat	gtc	caa	ata	agc	aca	cca	cgc	cca	gtc	720
Gln	Thr	Asn	Thr	Ile	Ile	Asp	Val	Gln	Ile	Ser	Thr	Pro	Arg	Pro	Val	
225					230					235					240	
aaa	tta	ctt	aga	ggc	cat	act	ctt	gtc	ctc	aat	tgt	act	gct	acc	act	768
Lys	Leu	Leu	Arg	Gly	His	Thr	Leu	Val	Leu	Asn	Cys	Thr	Ala	Thr	Thr	
				245				250						255		
ccc	ttg	aac	acg	aga	gtt	caa	atg	acc	tgg	agt	tac	cct	gat	gaa	aaa	816
Pro	Leu	Asn	Thr	Arg	Val	Gln	Met	Thr	Trp	Ser	Tyr	Pro	Asp	Glu	Lys	
			260					265					270			
aat	aag	aga	gct	tcc	gta	agg	cga	cga	att	gac	caa	agc	aat	tcc	cat	864
Asn	Lys	Arg	Ala	Ser	Val	Arg	Arg	Arg	Ile	Asp	Gln	Ser	Asn	Ser	His	
		275					280					285				
gcc	aac	ata	ttc	tac	agt	gtt	ctt	act	att	gac	aaa	atg	cag	aac	aaa	912
Ala	Asn	Ile	Phe	Tyr	Ser	Val	Leu	Thr	Ile	Asp	Lys	Met	Gln	Asn	Lys	
	290					295					300					
gac	aaa	gga	ctt	tat	act	tgt	cgt	gta	agg	agt	gga	cca	tca	ttc	aaa	960
Asp	Lys	Gly	Leu	Tyr	Thr	Cys	Arg	Val	Arg	Ser	Gly	Pro	Ser	Phe	Lys	
305					310					315					320	
tct	gtt	aac	acc	tca	gtg	cat	ata	tat	gat	aaa	gca	ggc	ccg	ggc	gag	1008
Ser	Val	Asn	Thr	Ser	Val	His	Ile	Tyr	Asp	Lys	Ala	Gly	Pro	Gly	Glu	
				325					330					335		
ccc	aaa	tct	tgt	gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	1056
Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	
			340					345					350			
gaa	ctc	ctg	ggg	gga	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	1104
Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	
		355					360					365				
gac	acc	ctc	atg	atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	1152
Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	
	370					375					380					

gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp 385 390 395 400	1200
ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr 405 410 415	1248
aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp 420 425 430	1296
tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu 435 440 445	1344
cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg 450 455 460	1392
gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys 465 470 475 480	1440
aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp 485 490 495	1488
atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys 500 505 510	1536
acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser 515 520 525	1584
aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser 530 535 540	1632
tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser 545 550 555 560	1680
ctc tcc ctg tct ccg ggt aaa tga Leu Ser Leu Ser Pro Gly Lys 565	1704

<210> 12
 <211> 567
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Flt(1-3)-Fc

<400> 12

Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
1 5 10 15

Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro
 20 25 30

Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr
 35 40 45

Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro
 50 55 60

Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala
 65 70 75 80

Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr
 85 90 95

Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val
 100 105 110

Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile
 115 120 125

Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu
 130 135 140

Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val
 145 150 155 160

Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr
 165 170 175

Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe
 180 185 190

Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu
 195 200 205

Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg
 210 215 220

Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val
 225 230 235 240

Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr
 245 250 255

Pro Leu Asn Thr Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys
260 265 270

Asn Lys Arg Ala Ser Val Arg Arg Arg Ile Asp Gln Ser Asn Ser His
275 280 285

Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys
290 295 300

Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys
305 310 315 320

Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu
325 330 335

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
340 345 350

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
355 360 365

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
370 375 380

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
385 390 395 400

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
405 410 415

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
420 425 430

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
435 440 445

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
450 455 460

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
465 470 475 480

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
485 490 495

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
500 505 510

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
515 520 525

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
530 535 540

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
545 550 555 560

Leu Ser Leu Ser Pro Gly Lys
565

<210> 13
<211> 1674
<212> DNA
<213> Artificial Sequence

<220>
<223> Flt1(1-3 ~~deltaB~~) (Mut 1)

<220>
<221> CDS
<222> (1)..(1674).

<400> 13
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tgt ctg ctt ctc aca gga tct agt tca ggt tca aaa tta aaa gat cct 96
Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro
20 25 30
gaa ctg agt tta aaa ggc acc cag cac atc atg caa gca ggc cag aca 144
Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr
35 40 45
ctg cat ctc caa tgc agg ggg gaa gca gcc cat aaa tgg tct ttg cct 192
Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro
50 55 60
gaa atg gtg agt aag gaa agc gaa agg ctg agc ata act aaa tct gcc 240
Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala
65 70 75 80
tgt gga aga aat ggc aaa caa ttc tgc agt act tta acc ttg aac aca 288
Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr
85 90 95
gct caa gca aac cac act ggc ttc tac agc tgc aaa tat cta gct gta 336
Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val
100 105 110

cct act tca aag aag aag gaa aca gaa tct gca atc tat ata ttt att Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile 115 120 125	384
agt gat aca ggt aga cct ttc gta gag atg tac agt gaa atc ccc gaa Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu 130 135 140	432
att ata cac atg act gaa gga agg gag ctc gtc att ccc tgc cgg gtt Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val 145 150 155 160	480
acg tca cct aac atc act gtt act tta aaa aag ttt cca ctt gac act Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr 165 170 175	528
ttg atc cct gat gga aaa cgc ata atc tgg gac agt aga aag ggc ttc Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe 180 185 190	576
atc ata tca aat gca acg tac aaa gaa ata ggg ctt ctg acc tgt gaa Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu 195 200 205	624
gca aca gtc aat ggg cat ttg tat aag aca aac tat ctc aca cat cga Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg 210 215 220	672
caa acc aat aca atc ata gat gtc caa ata agc aca cca cgc cca gtc Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val 225 230 235 240	720
aaa tta ctt aga ggc cat act ctt gtc ctc aat tgt act gct acc act Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr 245 250 255	768
ccc ttg aac acg aga gtt caa atg acc tgg agt tac cct gat gaa att Pro Leu Asn Thr Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Ile 260 265 270	816
gac caa agc aat tcc cat gcc aac ata ttc tac agt gtt ctt act att Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile 275 280 285	864
gac aaa atg cag aac aaa gac aaa gga ctt tat act tgt cgt gta agg Asp Lys Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg 290 295 300	912
agt gga cca tca ttc aaa tct gtt aac acc tca gtg cat ata tat gat Ser Gly Pro Ser Phe Lys Ser Val Asn Thr Ser Val His Ile Tyr Asp 305 310 315 320	960
aaa gca ggc ccg ggc gag ccc aaa tct tgt gac aaa act cac aca tgc Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys 325 330 335	1008
cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu 340 345 350	1056
ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag	1104

Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu		
		355					360					365					
gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	gaa	gac	cct	gag	gtc	aag	1152	
Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys		
	370					375					380						
ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	cat	aat	gcc	aag	aca	aag	1200	
Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys		
385					390					395					400		
ccg	cgg	gag	gag	cag	tac	aac	agc	acg	tac	cgt	gtg	gtc	agc	gtc	ctc	1248	
Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu		
				405					410					415			
acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc	aag	gag	tac	aag	tgc	aag	1296	
Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys		
			420					425					430				
gtc	tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	atc	gag	aaa	acc	atc	tcc	aaa	1344	
Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys		
		435					440					445					
gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	tac	acc	ctg	ccc	cca	tcc	1392	
Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser		
	450					455					460						
cgg	gat	gag	ctg	acc	aag	aac	cag	gtc	agc	ctg	acc	tgc	ctg	gtc	aaa	1440	
Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys		
465					470				475						480		
ggc	ttc	tat	ccc	agc	gac	atc	gcc	gtg	gag	tgg	gag	agc	aat	ggg	cag	1488	
Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln		
				485				490						495			
ccg	gag	aac	aac	tac	aag	acc	acg	cct	ccc	gtg	ctg	gac	tcc	gac	ggc	1536	
Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly		
			500					505					510				
tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	gac	aag	agc	agg	tgg	cag	1584	
Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln		
		515					520					525					
cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	cat	gag	gct	ctg	cac	aac	1632	
Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn		
	530					535					540						
cac	tac	acg	cag	aag	agc	ctc	tcc	ctg	tct	ccg	ggg	aaa	tga			1674	
His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys					
545					550					555							

<210> 14
 <211> 557
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Flt1(1-3 *deltaB*)-Fc (Mut1)

 <400> 14

Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
 1 5 10 15
 Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro
 20 25 30
 Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr
 35 40 45
 Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro
 50 55 60
 Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala
 65 70 75 80
 Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr
 85 90 95
 Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val
 100 105 110
 Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile
 115 120 125
 Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu
 130 135 140
 Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val
 145 150 155 160
 Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr
 165 170 175
 Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe
 180 185 190
 Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu
 195 200 205
 Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg
 210 215 220
 Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val
 225 230 235 240

Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr
 245 250 255

Pro Leu Asn Thr Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Ile
 260 265 270

Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile
 275 280 285

Asp Lys Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg
 290 295 300

Ser Gly Pro Ser Phe Lys Ser Val Asn Thr Ser Val His Ile Tyr Asp
 305 310 315 320

Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
 325 330 335

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
 340 345 350

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 355 360 365

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
 370 375 380

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 385 390 395 400

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 405 410 415

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 420 425 430

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
 435 440 445

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
 450 455 460

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 465 470 475 480

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln

485

490

495

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
500 505 510

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
515 520 525

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
530 535 540

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
545 550 555

<210> 15
<211> 1359
<212> DNA
<213> Artificial Sequence

<220>
<223> Flt1(2-3_{deltaB})-Fc(Mut2)

<220>
<221> CDS
<222> (1)..(1359)

<400> 15
atg gtc agc tac tgg gac acc ggg gtc ctg ctg tgc gcg ctg ctc agc 48
Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
1 5 10 15

tgt ctg ctt ctc aca gga tct agt tcc gga ggt aga cct ttc gta gag 96
Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Gly Arg Pro Phe Val Glu
20 25 30

atg tac agt gaa atc ccc gaa att ata cac atg act gaa gga agg gag 144
Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu
35 40 45

ctc gtc att ccc tgc cgg gtt acg tca cct aac atc act gtt act tta 192
Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu
50 55 60

aaa aag ttt cca ctt gac act ttg atc cct gat gga aaa cgc ata atc 240
Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile
65 70 75 80

tgg gac agt aga aag ggc ttc atc ata tca aat gca acg tac aaa gaa 288
Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu
85 90 95

ata ggg ctt ctg acc tgt gaa gca aca gtc aat ggg cat ttg tat aag 336
Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys
100 105 110

aca aac tat ctc aca cat cga caa acc aat aca atc ata gat gtc caa 384
Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln

115	120	125	
ata agc aca cca cgc cca gtc	aaa tta ctt aga ggc	cat act ctt gtc	432
Ile Ser Thr Pro Arg Pro Val	Lys Leu Leu Arg Gly	His Thr Leu Val	
130	135	140	
ctc aat tgt act gct acc act	ccc ttg aac acg aga gtt	caa atg acc	480
Leu Asn Cys Thr Ala Thr Thr	Pro Leu Asn Thr Arg Val	Gln Met Thr	
145	150	155	160
tgg agt tac cct gat gaa att	gac caa agc aat tcc cat	gcc aac ata	528
Trp Ser Tyr Pro Asp Glu Ile	Asp Gln Ser Asn Ser His	Ala Asn Ile	
165	170	175	
ttc tac agt gtt ctt act att	gac aaa atg cag aac aaa	gac aaa gga	576
Phe Tyr Ser Val Leu Thr Ile	Asp Lys Met Gln Asn Lys	Asp Lys Gly	
180	185	190	
ctt tat act tgt cgt gta agg	agt gga cca tca ttc aaa	tct gtt aac	624
Leu Tyr Thr Cys Arg Val Arg	Ser Gly Pro Ser Phe Lys	Ser Val Asn	
195	200	205	
acc tca gtg cat ata tat gat	aaa gca ggc ccg ggc gag	ccc aaa tct	672
Thr Ser Val His Ile Tyr Asp	Lys Ala Gly Pro Gly Glu	Pro Lys Ser	
210	215	220	
tgt gac aaa act cac aca tgc	cca ccg tgc cca gca cct	gaa ctc ctg	720
Cys Asp Lys Thr His Thr Cys	Pro Pro Cys Pro Ala Pro	Glu Leu Leu	
225	230	235	240
ggg gga ccg tca gtc ttc ctc	ttc ccc cca aaa ccc aag	gac acc ctc	768
Gly Gly Pro Ser Val Phe Leu	Phe Pro Pro Lys Pro Lys	Asp Thr Leu	
245	250	255	
atg atc tcc cgg acc cct gag	gtc aca tgc gtg gtg gtg	gac gtg agc	816
Met Ile Ser Arg Thr Pro Glu	Val Thr Cys Val Val Val	Asp Val Ser	
260	265	270	
cac gaa gac cct gag gtc aag	ttc aac tgg tac gtg gac	ggc gtg gag	864
His Glu Asp Pro Glu Val Lys	Phe Asn Trp Tyr Val Asp	Gly Val Glu	
275	280	285	
gtg cat aat gcc aag aca aag	ccg cgg gag gag cag tac	aac agc acg	912
Val His Asn Ala Lys Thr Lys	Pro Arg Glu Glu Gln Tyr	Asn Ser Thr	
290	295	300	
tac cgt gtg gtc agc gtc ctc	acc gtc ctg cac cag gac	tgg ctg aat	960
Tyr Arg Val Val Ser Val Leu	Thr Val Leu His Gln Asp	Trp Leu Asn	
305	310	315	320
ggc aag gag tac aag tgc aag	gtc tcc aac aaa gcc ctc	cca gcc ccc	1008
Gly Lys Glu Tyr Lys Cys Lys	Val Ser Asn Lys Ala Leu	Pro Ala Pro	
325	330	335	
atc gag aaa acc atc tcc aaa	gcc aaa ggg cag ccc cga	gaa cca cag	1056
Ile Glu Lys Thr Ile Ser Lys	Ala Lys Gly Gln Pro Arg	Glu Pro Gln	
340	345	350	
gtg tac acc ctg ccc cca tcc	cgg gat gag ctg acc aag	aac cag gtc	1104
Val Tyr Thr Leu Pro Pro Ser	Arg Asp Glu Leu Thr Lys	Asn Gln Val	
355	360	365	

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg	1152
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val	
370 375 380	
gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct	1200
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro	
385 390 395 400	
ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc	1248
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr	
405 410 415	
gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg	1296
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val	
420 425 430	
atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg	1344
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu	
435 440 445	
tct ccg ggt aaa tga	1359
Ser Pro Gly Lys	
450	

<210> 16
 <211> 452
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Flt1(2-3 ^{del}tab)-FC

<400> 16

Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser	
1 5 10 15	
Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Gly Arg Pro Phe Val Glu	
20 25 30	
Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu	
35 40 45	
Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu	
50 55 60	
Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile	
65 70 75 80	
Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu	
85 90 95	
Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys	

100	105	110
Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln 115 120 125		
Ile Ser Thr Pro Arg Pro Val Lys Leu Leu Arg Gly His Thr Leu Val 130 135 140		
Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr Arg Val Gln Met Thr 145 150 155 160		
Trp Ser Tyr Pro Asp Glu Ile Asp Gln Ser Asn Ser His Ala Asn Ile 165 170 175		
Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys Asp Lys Gly 180 185 190		
Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys Ser Val Asn 195 200 205		
Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu Pro Lys Ser 210 215 220		
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu 225 230 235 240		
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu 245 250 255		
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser 260 265 270		
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu 275 280 285		
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr 290 295 300		
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn 305 310 315 320		
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro 325 330 335		
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln 340 345 350		

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 355 360 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 385 390 395 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 405 410 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 435 440 445

Ser Pro Gly Lys
 450

<210> 17
 <211> 1389
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Flt1(2-3)-Fc (Mut3)

<220>
 <221> CDS
 <222> (1)..(1389)

<400> 17
 atg gtc agc tac tgg gac acc ggg gtc ctg ctg tgc gcg ctg ctc agc 48
 Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
 1 5 10 15
 tgt ctg ctt ctc aca gga tct agt tcc gga ggt aga cct ttc gta gag 96
 Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Gly Arg Pro Phe Val Glu
 20 25 30
 atg tac agt gaa atc ccc gaa att ata cac atg act gaa gga agg gag 144
 Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu
 35 40 45
 ctc gtc att ccc tgc cgg gtt acg tca cct aac atc act gtt act tta 192
 Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu
 50 55 60
 aaa aag ttt cca ctt gac act ttg atc cct gat gga aaa cgc ata atc 240
 Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile

65	70					75					80					
tgg gac agt aga aag ggc ttc atc ata tca aat gca acg tac aaa gaa	Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu					90					95					288
Trp Asp Ser Arg	85															
ata ggg ctt ctg acc tgt gaa gca aca gtc aat ggg cat ttg tat aag	Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys					105					110					336
Ile	100															
aca aac tat ctc aca cat cga caa acc aat aca atc ata gat gtc caa	Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln					120					125					384
Thr	115															
ata agc aca cca cgc cca gtc aaa tta ctt aga ggc cat act ctt gtc	Ile Ser Thr Pro Arg Pro Val Lys Leu Leu Arg Gly His Thr Leu Val					135					140					432
Ile	130															
ctc aat tgt act gct acc act ccc ttg aac acg aga gtt caa atg acc	Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr Arg Val Gln Met Thr					150					155					480
Leu	145															
tgg agt tac cct gat gaa aaa aat aag aga gct tcc gta agg cga cga	Trp Ser Tyr Pro Asp Glu Lys Asn Lys Arg Ala Ser Val Arg Arg Arg					165					170					528
Trp	165															
att gac caa agc aat tcc cat gcc aac ata ttc tac agt gtt ctt act	Ile Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr					185					190					576
Ile	180															
att gac aaa atg cag aac aaa gac aaa gga ctt tat act tgt cgt gta	Ile Asp Lys Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val					200					205					624
Ile	195															
agg agt gga cca tca ttc aaa tct gtt aac acc tca gtg cat ata tat	Arg Ser Gly Pro Ser Phe Lys Ser Val Asn Thr Ser Val His Ile Tyr					215					220					672
Arg	210															
gat aaa gca ggc ccg ggc gag ccc aaa tct tgt gac aaa act cac aca	Asp Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys Asp Lys Thr His Thr					230					235					720
Asp	225															
tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc	Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe					245					250					768
Cys	245															
ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct	Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro					265					270					816
Leu	260															
gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc	Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val					280					285					864
Glu	275															
aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca	Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr					295					300					912
Lys	290															
aag ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc	Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Arg Val Val Ser Val					310					315					960
Lys	305															

ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc	1008
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys	
325 330 335	
aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc	1056
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser	
340 345 350	
aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca	1104
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro	
355 360 365	
tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc	1152
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val	
370 375 380	
aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg	1200
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly	
385 390 395 400	
cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac	1248
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp	
405 410 415	
ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg	1296
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp	
420 425 430	
cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac	1344
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His	
435 440 445	
aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga	1389
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys	
450 455 460	

<210> 18
 <211> 462
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Flt1(2-3)-Fc (Mut3)

<400> 18

Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
1 5 10 15

Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Gly Arg Pro Phe Val Glu
20 25 30

Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu
35 40 45

Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu

50

55

60

Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile
65 70 75 80

Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu
85 90 95

Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys
100 105 110

Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln
115 120 125

Ile Ser Thr Pro Arg Pro Val Lys Leu Leu Arg Gly His Thr Leu Val
130 135 140

Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr Arg Val Gln Met Thr
145 150 155 160

Trp Ser Tyr Pro Asp Glu Lys Asn Lys Arg Ala Ser Val Arg Arg Arg
165 170 175

Ile Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr
180 185 190

Ile Asp Lys Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val
195 200 205

Arg Ser Gly Pro Ser Phe Lys Ser Val Asn Thr Ser Val His Ile Tyr
210 215 220

Asp Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys Asp Lys Thr His Thr
225 230 235 240

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
245 250 255

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
260 265 270

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
275 280 285

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
290 295 300

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 305 310 315 320

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 325 330 335

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 340 345 350

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 355 360 365

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 370 375 380

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 385 390 395 400

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 405 410 415

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 420 425 430

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 435 440 445

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 450 455 460

<210> 19
 <211> 1704
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Flt1(1-3 R->N) (Mut 4)

<220>
 <221> CDS
 <222> (1)..(1704)

<400> 19
 atg gtc agc tac tgg gac acc ggg gtc ctg ctg tgc gcg ctg ctc agc 48
 Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
 1 5 10 15

tgt ctg ctt ctc aca gga tct agt tca ggt tca aaa tta aaa gat cct 96
 Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro

20					25					30						
gaa	ctg	agt	tta	aaa	ggc	acc	cag	cac	atc	atg	caa	gca	ggc	cag	aca	144
Glu	Leu	Ser	Leu	Lys	Gly	Thr	Gln	His	Ile	Met	Gln	Ala	Gly	Gln	Thr	
	35						40					45				
ctg	cat	ctc	caa	tgc	agg	ggg	gaa	gca	gcc	cat	aaa	tgg	tct	ttg	cct	192
Leu	His	Leu	Gln	Cys	Arg	Gly	Glu	Ala	Ala	His	Lys	Trp	Ser	Leu	Pro	
	50					55					60					
gaa	atg	gtg	agt	aag	gaa	agc	gaa	agg	ctg	agc	ata	act	aaa	tct	gcc	240
Glu	Met	Val	Ser	Lys	Glu	Ser	Glu	Arg	Leu	Ser	Ile	Thr	Lys	Ser	Ala	
65					70					75					80	
tgt	gga	aga	aat	ggc	aaa	caa	ttc	tgc	agt	act	tta	acc	ttg	aac	aca	288
Cys	Gly	Arg	Asn	Gly	Lys	Gln	Phe	Cys	Ser	Thr	Leu	Thr	Leu	Asn	Thr	
				85					90					95		
gct	caa	gca	aac	cac	act	ggc	ttc	tac	agc	tgc	aaa	tat	cta	gct	gta	336
Ala	Gln	Ala	Asn	His	Thr	Gly	Phe	Tyr	Ser	Cys	Lys	Tyr	Leu	Ala	Val	
			100					105					110			
cct	act	tca	aag	aag	aag	gaa	aca	gaa	tct	gca	atc	tat	ata	ttt	att	384
Pro	Thr	Ser	Lys	Lys	Lys	Glu	Thr	Glu	Ser	Ala	Ile	Tyr	Ile	Phe	Ile	
		115					120					125				
agt	gat	aca	ggc	aga	cct	ttc	gta	gag	atg	tac	agt	gaa	atc	ccc	gaa	432
Ser	Asp	Thr	Gly	Arg	Pro	Phe	Val	Glu	Met	Tyr	Ser	Glu	Ile	Pro	Glu	
	130					135					140					
att	ata	cac	atg	act	gaa	gga	agg	gag	ctc	gtc	att	ccc	tgc	cgg	gtt	480
Ile	Ile	His	Met	Thr	Glu	Gly	Arg	Glu	Leu	Val	Ile	Pro	Cys	Arg	Val	
145					150					155					160	
acg	tca	cct	aac	atc	act	gtt	act	tta	aaa	aag	ttt	cca	ctt	gac	act	528
Thr	Ser	Pro	Asn	Ile	Thr	Val	Thr	Leu	Lys	Lys	Phe	Pro	Leu	Asp	Thr	
				165					170					175		
ttg	atc	cct	gat	gga	aaa	cgc	ata	atc	tgg	gac	agt	aga	aag	ggc	ttc	576
Leu	Ile	Pro	Asp	Gly	Lys	Arg	Ile	Ile	Trp	Asp	Ser	Arg	Lys	Gly	Phe	
			180					185					190			
atc	ata	tca	aat	gca	acg	tac	aaa	gaa	ata	ggg	ctt	ctg	acc	tgt	gaa	624
Ile	Ile	Ser	Asn	Ala	Thr	Tyr	Lys	Glu	Ile	Gly	Leu	Leu	Thr	Cys	Glu	
		195					200					205				
gca	aca	gtc	aat	ggg	cat	ttg	tat	aag	aca	aac	tat	ctc	aca	cat	cga	672
Ala	Thr	Val	Asn	Gly	His	Leu	Tyr	Lys	Thr	Asn	Tyr	Leu	Thr	His	Arg	
	210					215					220					
caa	acc	aat	aca	atc	ata	gat	gtc	caa	ata	agc	aca	cca	cgc	cca	gtc	720
Gln	Thr	Asn	Thr	Ile	Ile	Asp	Val	Gln	Ile	Ser	Thr	Pro	Arg	Pro	Val	
225					230					235					240	
aaa	tta	ctt	aga	ggc	cat	act	ctt	gtc	ctc	aat	tgt	act	gct	acc	act	768
Lys	Leu	Leu	Arg	Gly	His	Thr	Leu	Val	Leu	Asn	Cys	Thr	Ala	Thr	Thr	
				245					250					255		
ccc	ttg	aac	acg	aga	gtt	caa	atg	acc	tgg	agt	tac	cct	gat	gaa	aaa	816
Pro	Leu	Asn	Thr	Arg	Val	Gln	Met	Thr	Trp	Ser	Tyr	Pro	Asp	Glu	Lys	
			260					265					270			

aat aag aac gct tcc gta agg cga cga att gac caa agc aat tcc cat	864
Asn Lys Asn Ala Ser Val Arg Arg Arg Ile Asp Gln Ser Asn Ser His	
275 280 285	
gcc aac ata ttc tac agt gtt ctt act att gac aaa atg cag aac aaa	912
Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys	
290 295 300	
gac aaa gga ctt tat act tgt cgt gta agg agt gga cca tca ttc aaa	960
Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys	
305 310 315 320	
tct gtt aac acc tca gtg cat ata tat gat aaa gca ggc ccg ggc gag	1008
Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu	
325 330 335	
ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct	1056
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro	
340 345 350	
gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag	1104
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys	
355 360 365	
gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg	1152
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val	
370 375 380	
gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac	1200
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp	
385 390 395 400	
ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac	1248
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr	
405 410 415	
aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac	1296
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp	
420 425 430	
tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc	1344
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu	
435 440 445	
cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga	1392
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg	
450 455 460	
gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag	1440
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys	
465 470 475 480	
aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac	1488
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp	
485 490 495	
atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag	1536
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys	
500 505 510	

acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc 1584
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 515 520 525

aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca 1632
 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 530 535 540

tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc 1680
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 545 550 555 560

ctc tcc ctg tct ccg ggt aaa tga 1704
 Leu Ser Leu Ser Pro Gly Lys
 565

<210> 20
 <211> 567
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Flt1(1-3_{R->N})-Fc (Mut4)

<400> 20

Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
 1 5 10 15

Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro
 20 25 30

Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly Gln Thr
 35 40 45

Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser Leu Pro
 50 55 60

Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala
 65 70 75 80

Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr
 85 90 95

Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val
 100 105 110

Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile Phe Ile
 115 120 125

Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu
 130 135 140

Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val
 145 150 155 160

Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr
 165 170 175

Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe
 180 185 190

Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu
 195 200 205

Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg
 210 215 220

Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val
 225 230 235 240

Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr
 245 250 255

Pro Leu Asn Thr Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys
 260 265 270

Asn Lys Asn Ala Ser Val Arg Arg Arg Ile Asp Gln Ser Asn Ser His
 275 280 285

Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys
 290 295 300

Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys
 305 310 315 320

Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu
 325 330 335

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
 340 345 350

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 355 360 365

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 370 375 380

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
385 390 395 400

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
405 410 415

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
420 425 430

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
435 440 445

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
450 455 460

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
465 470 475 480

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
485 490 495

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
500 505 510

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
515 520 525

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
530 535 540

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
545 550 555 560

Leu Ser Leu Ser Pro Gly Lys
565

<210> 21
<211> 1453
<212> DNA
<213> Artificial Sequence

<220>
<223> Flt1D2.Flk1D3.Fc_{delta}C1(a) Receptor

<220>
<221> CDS
<222> (69)..(1442)

<400> 21
aagcttgggc tgcaggtcga tgcactctag aggatcgatc cccgggagag ctcgaattcg 60
caaccacc atg gtc agc tac tgg gac acc ggg gtc ctg ctg tgc gcg ctg 110
Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu
1 5 10
ctc agc tgt ctg ctt ctc aca gga tct agt tcc gga ggt aga cct ttc 158
Leu Ser Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Gly Arg Pro Phe
15 20 25 30
gta gag atg tac agt gaa atc ccc gaa att ata cac atg act gaa gga 206
Val Glu Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly
35 40 45
agg gag ctc gtc att ccc tgc cgg gtt acg tca cct aac atc act gtt 254
Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val
50 55 60
act tta aaa aag ttt cca ctt gac act ttg atc cct gat gga aaa cgc 302
Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg
65 70 75
ata atc tgg gac agt aga aag ggc ttc atc ata tca aat gca acg tac 350
Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr
80 85 90
aaa gaa ata ggg ctt ctg acc tgt gaa gca aca gtc aat ggg cat ttg 398
Lys Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu
95 100 105 110
tat aag aca aac tat ctc aca cat cga caa acc aat aca atc ata gat 446
Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp
115 120 125
gtg gtt ctg agt ccg tct cat gga att gaa cta tct gtt gga gaa aag 494
Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu Lys
130 135 140
ctt gtc tta aat tgt aca gca aga act gaa cta aat gtg ggg att gac 542
Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile Asp
145 150 155
ttc aac tgg gaa tac cct tct tgc aag cat cag cat aag aaa ctt gta 590
Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu Val
160 165 170
aac cga gac cta aaa acc cag tct ggg agt gag atg aag aaa ttt ttg 638
Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe Leu
175 180 185 190
agc acc tta act ata gat ggt gta acc cgg agt gac caa gga ttg tac 686
Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu Tyr
195 200 205
acc tgt gca gca tcc agt ggg ctg atg acc aag aag aac agc aca ttt 734
Thr Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr Phe
210 215 220
gtc agg gtc cat gaa aag ggc ccg ggc gac aaa act cac aca tgc cca 782
Val Arg Val His Glu Lys Gly Pro Gly Asp Lys Thr His Thr Cys Pro

225	230	235	
ccg tgc cca gca cct gaa ctc	ctg ggg gga ccg tca gtc ttc ctc ttc		830
Pro Cys Pro Ala Pro Glu Leu	Leu Gly Gly Pro Ser Val Phe Leu Phe		
240	245 250		
ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc		878	
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val			
255	260 265 270		
aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc		926	
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe			
	275 280 285		
aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg		974	
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro			
	290 295 300		
cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc		1022	
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr			
	305 310 315		
gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc		1070	
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val			
	320 325 330		
tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc		1118	
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala			
	335 340 345 350		
aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg		1166	
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg			
	355 360 365		
gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc		1214	
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly			
	370 375 380		
ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg		1262	
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro			
	385 390 395		
gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc		1310	
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser			
	400 405 410		
ttc ttc ctc tat agc aag ctc acc gtg gac aag agc agg tgg cag cag		1358	
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln			
	415 420 425 430		
ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac		1406	
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His			
	435 440 445		
tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tgagcggccg c		1453	
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys			
	450 455		

<210> 22
<211> 458

<212> PRT
 <213> Artificial Sequence
 <220>
 <223> Flt1D2.Flk1D3.Fc_{delta}C1(a) Receptor
 <400> 22

Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
 1 5 10 15

Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Gly Arg Pro Phe Val Glu
 20 25 30

Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu
 35 40 45

Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu
 50 55 60

Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile
 65 70 75 80

Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu
 85 90 95

Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys
 100 105 110

Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Val
 115 120 125

Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu Lys Leu Val
 130 135 140

Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile Asp Phe Asn
 145 150 155 160

Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu Val Asn Arg
 165 170 175

Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe Leu Ser Thr
 180 185 190

Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu Tyr Thr Cys
 195 200 205

Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr Phe Val Arg

210		215		220
Val His Glu Lys Gly Pro Gly Asp Lys Thr His Thr Cys Pro Pro Cys				
225		230	235	240
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro				
	245	250		255
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys				
	260	265		270
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp				
	275	280		285
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu				
	290	295	300	
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu				
305		310	315	320
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn				
	325	330		335
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly				
	340	345		350
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu				
	355	360	365	
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr				
	370	375	380	
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn				
385		390	395	400
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe				
	405	410		415
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn				
	420	425		430
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr				
	435	440	445	
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys				
450		455		

<210> 23
 <211> 1444
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Flt1D2.VEGFR3D3.Fc_{delta}C1(a) Receptor

<220>
 <221> CDS
 <222> (69)..(1436)

<400> 23
 aagcttgggc tgcaggtcga tgcactctag aggatcgatc cccgggcgag ctccaattcg 60
 caaccacc atg gtc agc tac tgg gac acc ggg gtc ctg ctg tgc gcg ctg 110
 Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu
 1 5 10
 ctc agc tgt ctg ctt ctc aca gga tct agt tcc gga ggt aga cct ttc 158
 Leu Ser Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Gly Arg Pro Phe
 15 20 25 30
 gta gag atg tac agt gaa atc ccc gaa att ata cac atg act gaa gga 206
 Val Glu Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly
 35 40 45
 agg gag ctc gtc att ccc tgc cgg gtt acg tca cct aac atc act gtt 254
 Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val
 50 55 60
 act tta aaa aag ttt cca ctt gac act ttg atc cct gat gga aaa cgc 302
 Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg
 65 70 75
 ata atc tgg gac agt aga aag ggc ttc atc ata tca aat gca acg tac 350
 Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr
 80 85 90
 aaa gaa ata ggg ctt ctg acc tgt gaa gca aca gtc aat ggg cat ttg 398
 Lys Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu
 95 100 105 110
 tat aag aca aac tat ctc aca cat cga caa acc aat aca atc ata gat 446
 Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp
 115 120 125
 atc cag ctg ttg ccc agg aag tcg ctg gag ctg ctg gta ggg gag aag 494
 Ile Gln Leu Leu Pro Arg Lys Ser Leu Glu Leu Leu Val Gly Glu Lys
 130 135 140
 ctg gtc ctc aac tgc acc gtg tgg gct gag ttt aac tca ggt gtc acc 542
 Leu Val Leu Asn Cys Thr Val Trp Ala Glu Phe Asn Ser Gly Val Thr
 145 150 155
 ttt gac tgg gac tac cca ggg aag cag gca gag cgg ggt aag tgg gtg 590
 Phe Asp Trp Asp Tyr Pro Gly Lys Gln Ala Glu Arg Gly Lys Trp Val
 160 165 170

ccc gag cga cgc tcc caa cag acc cac aca gaa ctc tcc agc atc ctg Pro Glu Arg Arg Ser Gln Gln Thr His Thr Glu Leu Ser Ser Ile Leu 175 180 185 190	638
acc atc cac aac gtc agc cag cac gac ctg ggc tcg tat gtg tgc aag Thr Ile His Asn Val Ser Gln His Asp Leu Gly Ser Tyr Val Cys Lys 195 200 205	686
gcc aac aac ggc atc cag cga ttt cgg gag agc acc gag gtc att gtg Ala Asn Asn Gly Ile Gln Arg Phe Arg Glu Ser Thr Glu Val Ile Val 210 215 220	734
cat gaa aat ggc ccg ggc gac aaa act cac aca tgc cca ccg tgc cca His Glu Asn Gly Pro Gly Asp Lys Thr His Thr Cys Pro Pro Cys Pro 225 230 235	782
gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys 240 245 250	830
ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val 255 260 265 270	878
gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr 275 280 285	926
gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu 290 295 300	974
cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His 305 310 315	1022
cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys 320 325 330	1070
gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln 335 340 345 350	1118
ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu 355 360 365	1166
acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro 370 375 380	1214
agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn 385 390 395	1262
tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu 400 405 410	1310
tat agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc	1358

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 415 420 425 430
 ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag 1406
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 435 440 445
 aag agc ctc tcc ctg tct ccg ggt aaa tga gcggccgc 1444
 Lys Ser Leu Ser Leu Ser Pro Gly Lys
 450 455

<210> 24
 <211> 455
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Flt1D2.VEGFR3D3.Fc_{delta}C1(a)Receptor

<400> 24

Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
 1 5 10 15

Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Gly Arg Pro Phe Val Glu
 20 25 30

Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu
 35 40 45

Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu
 50 55 60

Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile
 65 70 75 80

Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu
 85 90 95

Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys
 100 105 110

Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Ile Gln
 115 120 125

Leu Leu Pro Arg Lys Ser Leu Glu Leu Leu Val Gly Glu Lys Leu Val
 130 135 140

Leu Asn Cys Thr Val Trp Ala Glu Phe Asn Ser Gly Val Thr Phe Asp
 145 150 155 160

Trp	Asp	Tyr	Pro	Gly	Lys	Gln	Ala	Glu	Arg	Gly	Lys	Trp	Val	Pro	Glu
				165				170						175	
Arg	Arg	Ser	Gln	Gln	Thr	His	Thr	Glu	Leu	Ser	Ser	Ile	Leu	Thr	Ile
			180					185					190		
His	Asn	Val	Ser	Gln	His	Asp	Leu	Gly	Ser	Tyr	Val	Cys	Lys	Ala	Asn
		195					200					205			
Asn	Gly	Ile	Gln	Arg	Phe	Arg	Glu	Ser	Thr	Glu	Val	Ile	Val	His	Glu
	210					215					220				
Asn	Gly	Pro	Gly	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro
225					230					235					240
Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys
				245					250					255	
Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val
			260					265					270		
Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp
		275					280					285			
Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr
	290					295					300				
Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp
305					310					315					320
Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu
				325					330					335	
Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg
			340					345					350		
Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys
		355					360					365			
Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp
	370					375					380				
Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys
385					390					395					400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
435 440 445

Leu Ser Leu Ser Pro Gly Lys
450 455

<210> 25
<211> 1377
<212> DNA
<213> Artificial Sequence

<220>
<223> VEGFR1R2.FC_{delta}C1(a) Receptor

<220>
<221> CDS
<222> (1)..(1377)

<400> 25
atg gtc agc tac tgg gac acc ggg gtc ctg ctg tgc gcg ctg ctc agc 48
Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser
1 5 10 15
tgt ctg ctt ctc aca gga tct agt tcc gga agt gat acc ggt aga cct 96
Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Asp Thr Gly Arg Pro
20 25 30
ttc gta gag atg tac agt gaa atc ccc gaa att ata cac atg act gaa 144
Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile Ile His Met Thr Glu
35 40 45
gga agg gag ctc gtc att ccc tgc cgg gtt acg tca cct aac atc act 192
Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile Thr
50 55 60
gtt act tta aaa aag ttt cca ctt gac act ttg atc cct gat gga aaa 240
Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys
65 70 75 80
cgc ata atc tgg gac agt aga aag ggc ttc atc ata tca aat gca acg 288
Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr
85 90 95
tac aaa gaa ata ggg ctt ctg acc tgt gaa gca aca gtc aat ggg cat 336
Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His
100 105 110
ttg tat aag aca aac tat ctc aca cat cga caa acc aat aca atc ata 384
Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile
115 120 125

gat	gtg	gtt	ctg	agt	ccg	tct	cat	gga	att	gaa	cta	tct	gtt	gga	gaa	432
Asp	Val	Val	Leu	Ser	Pro	Ser	His	Gly	Ile	Glu	Leu	Ser	Val	Gly	Glu	
130						135					140					
aag	ctt	gtc	tta	aat	tgt	aca	gca	aga	act	gaa	cta	aat	gtg	ggg	att	480
Lys	Leu	Val	Leu	Asn	Cys	Thr	Ala	Arg	Thr	Glu	Leu	Asn	Val	Gly	Ile	
145					150					155					160	
gac	ttc	aac	tgg	gaa	tac	cct	tct	tcg	aag	cat	cag	cat	aag	aaa	ctt	528
Asp	Phe	Asn	Trp	Glu	Tyr	Pro	Ser	Ser	Lys	His	Gln	His	Lys	Lys	Leu	
				165					170					175		
gta	aac	cga	gac	cta	aaa	acc	cag	tct	ggg	agt	gag	atg	aag	aaa	ttt	576
Val	Asn	Arg	Asp	Leu	Lys	Thr	Gln	Ser	Gly	Ser	Glu	Met	Lys	Lys	Phe	
			180					185					190			
ttg	agc	acc	tta	act	ata	gat	ggg	gta	acc	cgg	agt	gac	caa	gga	ttg	624
Leu	Ser	Thr	Leu	Thr	Ile	Asp	Gly	Val	Thr	Arg	Ser	Asp	Gln	Gly	Leu	
		195					200					205				
tac	acc	tgt	gca	gca	tcc	agt	ggg	ctg	atg	acc	aag	aag	aac	agc	aca	672
Tyr	Thr	Cys	Ala	Ala	Ser	Ser	Gly	Leu	Met	Thr	Lys	Lys	Asn	Ser	Thr	
	210					215					220					
ttt	gtc	agg	gtc	cat	gaa	aag	gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	720
Phe	Val	Arg	Val	His	Glu	Lys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	
225					230					235					240	
cca	gca	cct	gaa	ctc	ctg	ggg	gga	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	768
Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	
				245				250						255		
aaa	ccc	aag	gac	acc	ctc	atg	atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	816
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	
			260					265					270			
gtg	gtg	gtg	gac	gtg	agc	cac	gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	864
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	
		275					280					285				
tac	gtg	gac	ggc	gtg	gag	gtg	cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	912
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	
	290					295					300					
gag	cag	tac	aac	agc	acg	tac	cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	960
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	
305					310					315					320	
cac	cag	gac	tgg	ctg	aat	ggc	aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	1008
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	
				325				330						335		
aaa	gcc	ctc	cca	gcc	ccc	atc	gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	1056
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	
			340				345					350				
cag	ccc	cga	gaa	cca	cag	gtg	tac	acc	ctg	ccc	cca	tcc	cgg	gat	gag	1104
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	
		355					360					365				
ctg	acc	aag	aac	cag	gtc	agc	ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	1152

Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr		
370						375					380						
ccc	agc	gac	atc	gcc	gtg	gag	tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	1200	
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn		
385					390					395					400		
aac	tac	aag	acc	acg	cct	ccc	gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	1248	
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe		
				405					410					415			
ctc	tac	agc	aag	ctc	acc	gtg	gac	aag	agc	agg	tgg	cag	cag	ggg	aac	1296	
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn		
			420					425						430			
gtc	ttc	tca	tgc	tcc	gtg	atg	cat	gag	gct	ctg	cac	aac	cac	tac	acg	1344	
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr		
		435					440					445					
cag	aag	agc	ctc	tcc	ctg	tct	ccg	ggt	aaa	tga						1377	
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys								
	450					455											

<210> 26
 <211> 458
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> VEGFR1R2-FC_{delta}C1(a) Receptor

 <400> 26

Met	Val	Ser	Tyr	Trp	Asp	Thr	Gly	Val	Leu	Leu	Cys	Ala	Leu	Leu	Ser		
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Cys	Leu	Leu	Leu	Thr	Gly	Ser	Ser	Ser	Gly	Ser	Asp	Thr	Gly	Arg	Pro		
			20					25					30				
Phe	Val	Glu	Met	Tyr	Ser	Glu	Ile	Pro	Glu	Ile	Ile	His	Met	Thr	Glu		
		35					40					45					
Gly	Arg	Glu	Leu	Val	Ile	Pro	Cys	Arg	Val	Thr	Ser	Pro	Asn	Ile	Thr		
	50					55					60						
Val	Thr	Leu	Lys	Lys	Phe	Pro	Leu	Asp	Thr	Leu	Ile	Pro	Asp	Gly	Lys		
65					70					75					80		
Arg	Ile	Ile	Trp	Asp	Ser	Arg	Lys	Gly	Phe	Ile	Ile	Ser	Asn	Ala	Thr		
			85						90					95			
Tyr	Lys	Glu	Ile	Gly	Leu	Leu	Thr	Cys	Glu	Ala	Thr	Val	Asn	Gly	His		
			100					105					110				

Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr Asn Thr Ile Ile
 115 120 125

Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu
 130 135 140

Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile
 145 150 155 160

Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu
 165 170 175

Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe
 180 185 190

Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu
 195 200 205

Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr
 210 215 220

Phe Val Arg Val His Glu Lys Asp Lys Thr His Thr Cys Pro Pro Cys
 225 230 235 240

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 245 250 255

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 260 265 270

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 275 280 285

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 290 295 300

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 305 310 315 320

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 325 330 335

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 340 345 350

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
 355 360 365

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 370 375 380

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 385 390 395 400

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 405 410 415

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 420 425 430

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 435 440 445

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 450 455

<210> 27
 <211> 431
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide

<400> 27

Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile Ile His
 1 5 10 15

Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro
 20 25 30

Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro
 35 40 45

Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser
 50 55 60

Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val
 65 70 75 80

Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln Thr Asn
 85 90 95

Thr Ile Ile Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser
 100 105 110

Val Gly Glu Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn
 115 120 125

Val	Gly	Ile	Asp	Phe	Asn	Trp	Glu	Tyr	Pro	Ser	Ser	Lys	His	Gln	His		
130						135					140						
Lys	Lys	Leu	Val	Asn	Arg	Asp	Leu	Lys	Thr	Gln	Ser	Gly	Ser	Glu	Met		
145				150						155					160		
Lys	Lys	Phe	Leu	Ser	Thr	Leu	Thr	Ile	Asp	Gly	Val	Thr	Arg	Ser	Asp		
				165					170					175			
Gln	Gly	Leu	Tyr	Thr	Cys	Ala	Ala	Ser	Ser	Gly	Leu	Met	Thr	Lys	Lys		
			180					185					190				
Asn	Ser	Thr	Phe	Val	Arg	Val	His	Glu	Lys	Gly	Pro	Gly	Asp	Lys	Thr		
		195					200					205					
His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser		
		210				215						220					
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg		
225					230					235					240		
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro		
				245					250					255			
Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala		
			260					265					270				
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val		
		275					280					285					
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr		
		290				295					300						
Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr		
305					310					315					320		
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu		
				325					330					335			
Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Thr	Cys	Leu		
			340					345					350				
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn		
		355					360					365					
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser		
		370				375					380						
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg		
385					390					395					400		
Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu		
				405				410						415			
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys			
			420					425					430				